

## **Identification of a Gene Encoding Slow Skeletal Muscle Troponin T as a Novel Marker for Immortalization of Retinal Pigment Epithelial Cells**

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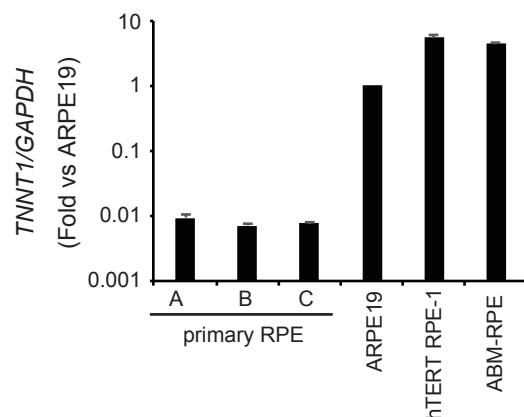
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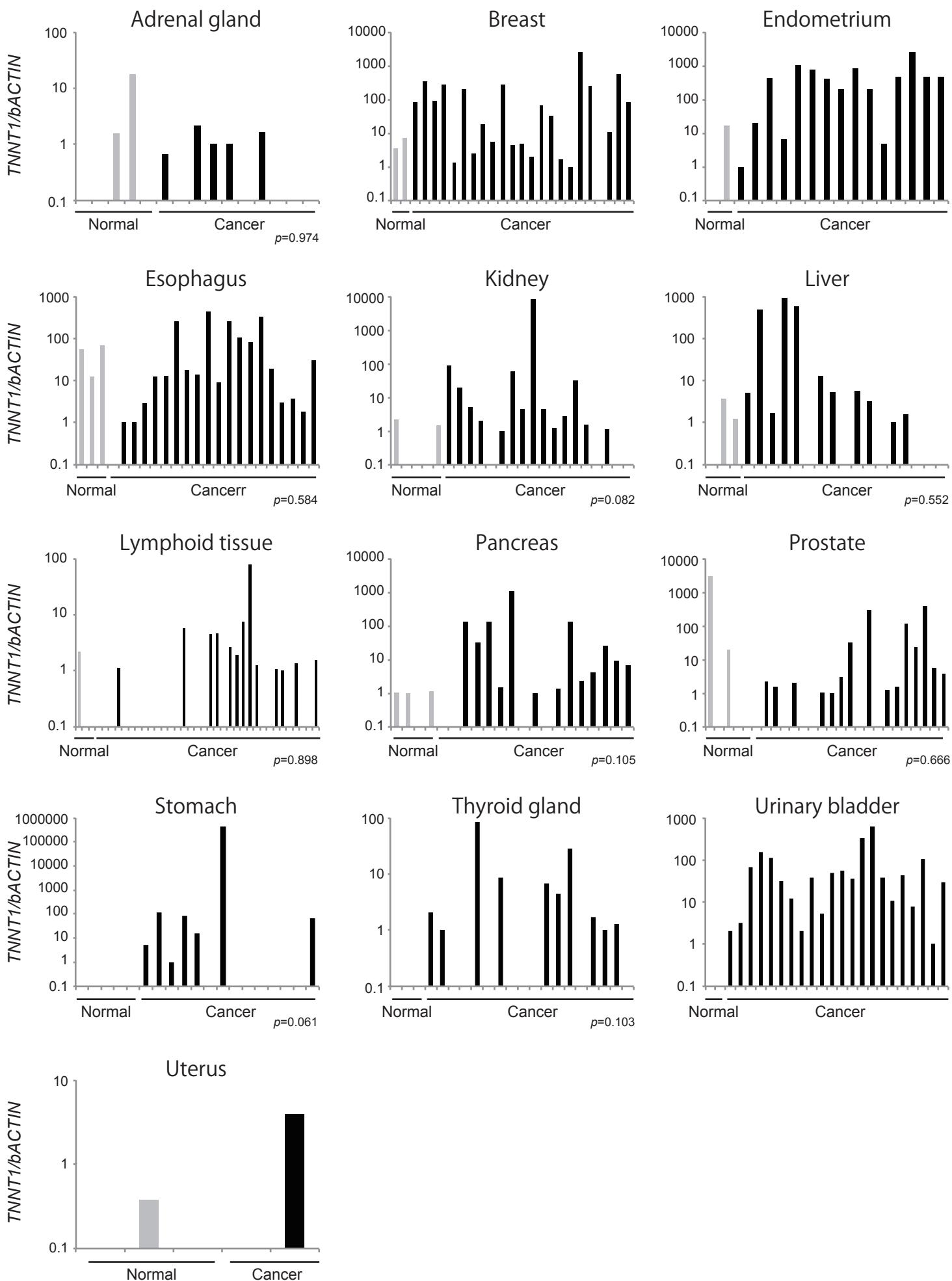
### **Supplementary Information**



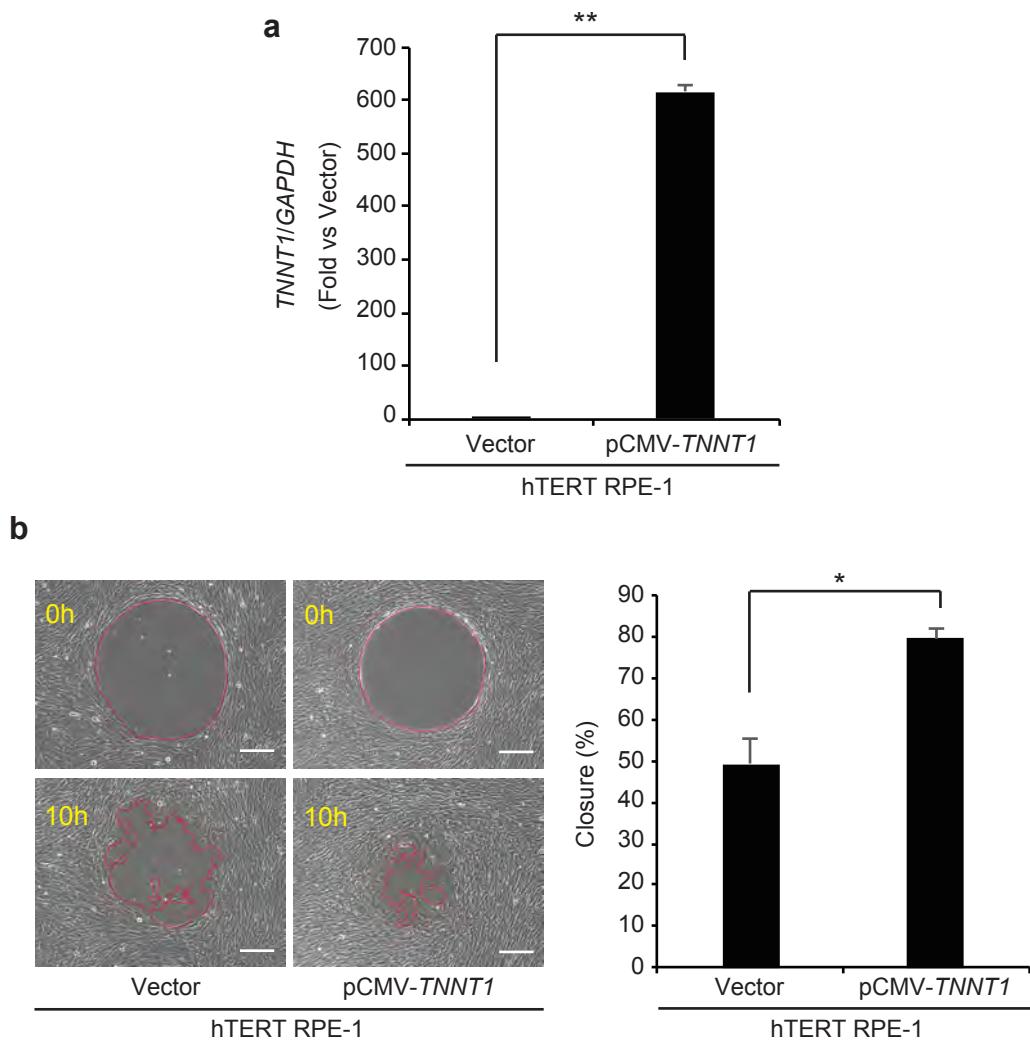
**Supplementary Figure 1. qRT-PCR analysis of *TNNT1* in immortalized RPE cell lines (hTERT RPE-1 and ABM-RPE).** Bar graph represents fold gene expression relative to ARPE-19 cells. Results are means  $\pm$  standard deviations ( $n = 3$ ).

Supplementary Figure 2

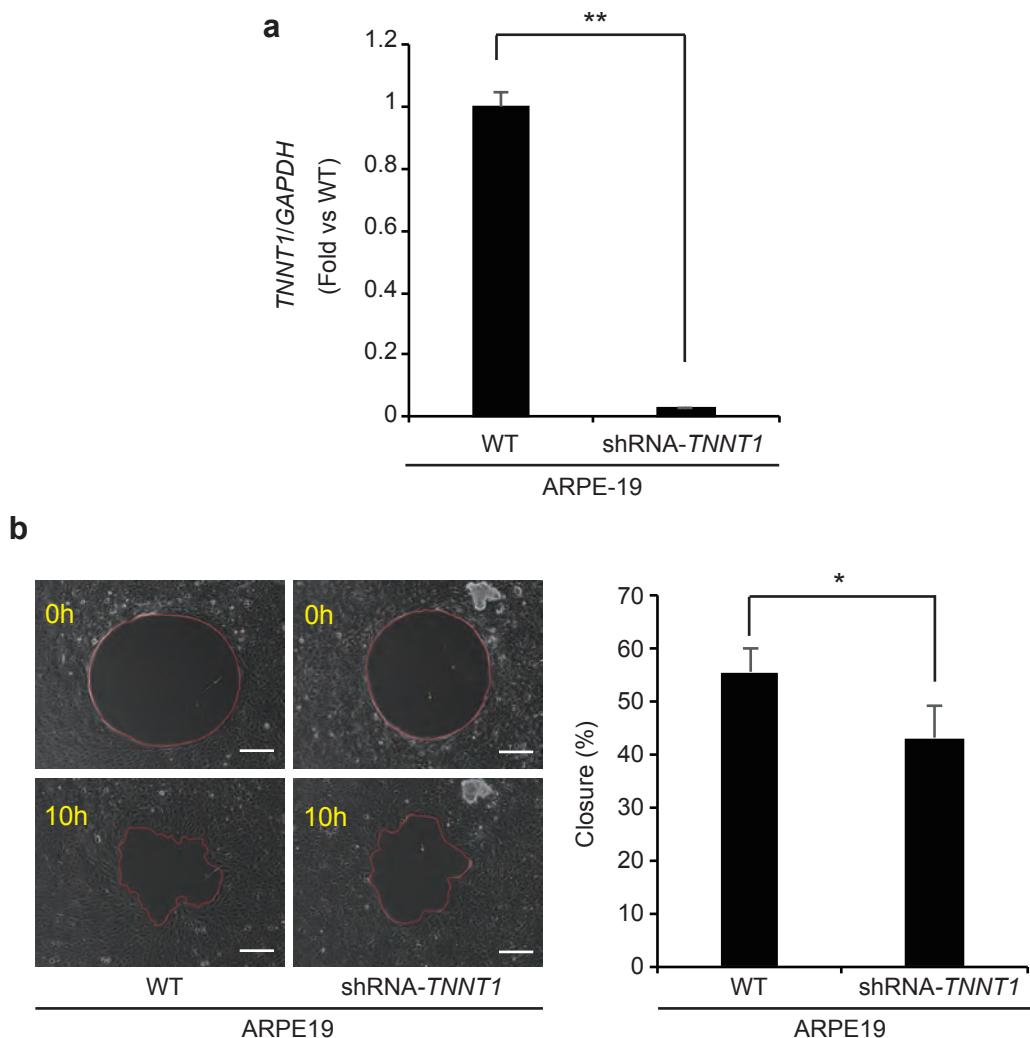
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**Supplementary Figure 2. The expression of *TNNT1* in various cancer tissues.** Expression profiles of *TNNT1* in human cancer tissues and normal tissues were quantified using the TissueScan Cancer Survey Panel. Data were obtained using the comparative CT method with the values normalized to  $\beta$ -actin levels. Bar graphs represented the fold expression of *TNNT1* relative to the lowest detected sample in cancer tissue samples (black; cancer tissue, gray; normal tissue). Blank: not detected. Statistical analyses of breast, endometrium, urinary bladder and uterus were not performed, because the number of the samples included in one group was less than three.



**Supplementary Figure 3. Overexpression of *TNNT1* enhances cell migration of hTERT RPE-1 cells.** (a) qRT-PCR analysis of *TNNT1* mRNA in hTERT RPE-1 cells (Vector) and pCMV-*TNNT1* hTERT RPE-1 cells (pCMV-*TNNT1*). Bar graph represents fold expression of *TNNT1* relative to sample of vector. (b) Phase-contrast images of migration assay of hTERT RPE1 cells (Vector) and pCMV-*TNNT1* hTERT RPE1 cells (pCMV-*TNNT1*). Scale bar: 200  $\mu$ m. Closure rates were calculated as described as material methods. Results are means  $\pm$  standard deviations ( $n = 3$ ). \* $P < 0.05$ , \*\* $P < 0.001$ , Student's t-test ( $n = 3$ )



**Supplementary Figure 4. Knockdown of *TNNT1* suppresses cell migration of ARPE19 cells.**

(A) qRT-PCR analysis of *TNNT1* mRNA in ARPE-19 cells (WT) and shRNA-*TNNT1* ARPE-19 cells (shRNA-*TNNT1*). Bar graph represents fold expression of *TNNT1* relative to ARPE-19 cells. (B) Phase-contrast images of migration assay of ARPE-19 cells (WT) and shRNA-*TNNT1* ARPE-19 cells (shRNA-*TNNT1*). Scale bar: 200  $\mu$ m. Closure rates were calculated as described as material methods. \* $P < 0.05$ , \*\* $P < 0.001$ , Student's t-test ( $n = 3$ )

**Supplementary Table 1. Probe and primer sequences**

Gene	Probe sequences (5' → 3')	Forward primer sequences (5' → 3')	Reverse primer sequences (5' → 3')
<i>TNNT1</i>	ATCCTCTCGAGCGTAAGAACGCTCTGG	GGGGCGGGAGATGAAGGTG	GGTCGAACCTCTCAGACTCCAG
<i>BDNF</i>	TTTCAAGGACTGTGACCCTCCGCC	GTGTGTGACAGTATTAGTGAGTGG	CTCGTAGAAGTATTGCTTCAGTTGG
<i>CAMK2NI</i>	TATGACCGACAAGGCACCTCTGGTG	CGGAGCAAGCGGGTTGTTA	CTCTCCCTTAACTCATTGTCTTGG
<i>CARD6</i>	ACCAAGTTATGAGGGATCAGAAACCAGCCT	CTTCGAGAAITCAGAAACCACAGAG	CCATGTTCAAACATAACAGGACATC
<i>CDH11</i>	TGCCAAAGACCCCTGATGCTGCCAACA	CACCGTGGTTGGGAGAGTG	TGTCGAGGTCACTGTGACGA
<i>CLDN11</i>	CCTTGTGCCACCATCTGGTTCCCTGTG	CTGGCTGGTGTGCTCATTC	TGGTGGTCTCACGGTGGG
<i>GADI</i>	CGAGGATGACCTGTGCGAACCCATACT	GGAGCAGATCCTGGTTGACTG	GCCAATAATCCAATCCAGTGGAG
<i>IL15</i>	TCCCTCAGTTCCCTCACATTCTTGATCCA	CATCCTAGCAAACAACAGTTGTC	TGGACAATATGTACAAAACCTTGCA
<i>PAPSS2</i>	TGGACCAATACCGTCTGACACCTCTGGA	TGCTGGAGAAAATAAGATGGAATGA	CGCAACTGGAATGCAAACACC
<i>PLK2</i>	TGCTACAGCTGCCAAGAGTCCCTCTGAC	CACCACAGTGGCAGGTCTG	GGTACTGTCTTCAGGCATTAC
<i>PGS1</i>	AGGTGAAACGTCCAGTTACTCCTCTAGTCC	ACACCTTACACATCATAAAGGGAGA	GGCTTAGGAGTCTCCAGGTG
<i>PGS4</i>	CGAGTTGTCCACCTCCAGCTTATAGGGC	AGCTCCAATCCATCACAGTCAA	GCTCACATGTCAGGTACAAGGG
<i>PGS7</i>	AGCTCCAATCCGTGACAGTCAGAGTCTCT	GCTTGCTCTGTCGTAACTCAG	GAGTGGGTCTGCTCTTGAGG
<i>SHOX2</i>	CAGTCGCTGGCTCAGTTCTCTCGCA	ACGAGACCCACTATCCGAC	CTTCGAITTGAAACCAAACCTGC
<i>TWIST1</i>	TCCAGCTCCAGAGTCTCTAGACTGTCCATT	GGCCGGAGACCTAGATGTCA	GGATTTGCTCTCTAATTCCAAGA

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*TERT* CAGCCTCCAGACGGTGTGCACCAAC CCTGTTCTGGATTGCAGGTG GCACACATGCGTGAAACCTG

*Survivin* CCTCGGCCATCCGCTCCGGG ACCACCGCATCTACATTCAAG CTCAGTGGGCAGTGGATGA

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